



## SEQUENCE LISTING

&lt;110&gt; Chang, Tai-Jay

<120> ANDROGEN RECEPTOR COMPLEX-ASSOCIATED  
PROTEIN

&lt;130&gt; 11709-003001

&lt;140&gt; US 09/781,693

&lt;141&gt; 2001-02-12

&lt;150&gt; US 60/262,312

&lt;151&gt; 2001-01-17

&lt;160&gt; 17

&lt;170&gt; FastSEQ for Windows Version 4.0

&lt;210&gt; 1

&lt;211&gt; 2580

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1

a!

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&lt;211&gt; 860

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

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Tyr	Ile	Leu	Ser	Gly	Ser	Asp	Asp	Thr	Lys	Leu	Val	Ile	Ser	Asn	Pro
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Tyr	Ser	Arg	Lys	Val	Leu	Thr	Thr	Ile	Arg	Ser	Gly	His	Arg	Ala	Asn
			85					90						95	
Ile	Phe	Ser	Ala	Lys	Phe	Leu	Pro	Cys	Thr	Asn	Asp	Lys	Gln	Ile	Val
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Ser	Cys	Ser	Gly	Asp	Gly	Val	Ile	Phe	Tyr	Thr	Asn	Val	Glu	Gln	Asp
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Tyr	Glu	Ile	Met	Thr	Val	Pro	Asn	Asp	Pro	Tyr	Thr	Phe	Leu	Ser	Cys
145					150					155					160
Gly	Glu	Asp	Gly	Thr	Val	Arg	Trp	Phe	Asp	Thr	Arg	Ile	Lys	Thr	Ser
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Cys	Thr	Lys	Glu	Asp	Cys	Lys	Asp	Asp	Ile	Leu	Ile	Asn	Cys	Arg	Arg
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Ala	Ala	Thr	Ser	Val	Ala	Ile	Cys	Pro	Pro	Ile	Pro	Tyr	Tyr	Leu	Ala
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Val	Gly	Cys	Ser	Asp	Ser	Ser	Val	Arg	Ile	Tyr	Asp	Arg	Arg	Met	Leu
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Gly	Thr	Arg	Ala	Thr	Gly	Asn	Tyr	Ala	Gly	Arg	Gly	Thr	Thr	Gly	Met
225					230					235					240
Val	Ala	Arg	Phe	Ile	Pro	Ser	His	Leu	Asn	Asn	Lys	Ser	Cys	Arg	Val
			245						250					255	
Thr	Ser	Leu	Cys	Tyr	Ser	Glu	Asp	Gly	Gln	Glu	Ile	Leu	Val	Ser	Tyr
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Ser	Ser	Asp	Tyr	Ile	Tyr	Leu	Phe	Asp	Pro	Lys	Asp	Asp	Thr	Ala	Arg
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Glu	Leu	Lys	Thr	Pro	Ser	Ala	Glu	Glu	Arg	Arg	Glu	Glu	Leu	Arg	Gln
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a!  
cont

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 Pro Arg Ala Arg Pro Glu Ser Glu Arg Glu Arg Asp Gly Glu Gln Ser  
 325 330 335  
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 340 345 350  
 Phe Glu Glu Ala Ser Glu Val Ala Gln Ser Asn Arg Gly Arg Gly Arg  
 355 360 365  
 Ser Arg Pro Arg Gly Gly Thr Ser Gln Ser Asp Ile Ser Thr Leu Pro  
 370 375 380  
 Thr Val Pro Ser Ser Pro Asp Leu Glu Val Ser Glu Thr Ala Met Glu  
 385 390 395 400  
 Val Asp Thr Pro Ala Glu Gln Phe Leu Gln Pro Ser Thr Ser Ser Thr  
 405 410 415  
 Met Ser Ala Gln Ala His Ser Thr Ser Ser Pro Thr Glu Ser Pro His  
 420 425 430  
 Ser Thr Pro Leu Leu Ser Ser Pro Asp Ser Glu Gln Arg Gln Ser Val  
 435 440 445  
 Glu Ala Ser Gly His His Thr His His Gln Ser Asp Asn Asn Asn Glu  
 450 455 460  
 Lys Leu Ser Pro Lys Pro Gly Thr Gly Glu Pro Val Leu Ser Leu His  
 465 470 475 480  
 Tyr Ser Thr Glu Gly Thr Thr Thr Ser Thr Ile Lys Leu Asn Phe Thr  
 485 490 495  
 Asp Glu Trp Ser Ser Ile Ala Ser Ser Ser Arg Gly Ile Gly Ser His  
 500 505 510  
 Cys Lys Ser Glu Gly Gln Glu Glu Ser Phe Val Pro Gln Ser Ser Val  
 515 520 525  
 Gln Pro Pro Glu Gly Asp Ser Glu Thr Lys Ala Pro Glu Glu Ser Ser  
 530 535 540  
 Glu Asp Val Thr Lys Tyr Gln Glu Gly Val Ser Ala Glu Asn Pro Val  
 545 550 555 560  
 Glu Asn His Ile Asn Ile Thr Gln Ser Asp Lys Phe Thr Ala Lys Pro  
 565 570 575  
 Leu Asp Ser Asn Ser Gly Glu Arg Asn Asp Leu Asn Leu Asp Arg Ser  
 580 585 590  
 Cys Gly Val Pro Glu Glu Ser Ala Ser Ser Glu Lys Ala Lys Glu Pro  
 595 600 605  
 Glu Thr Ser Asp Gln Thr Ser Thr Glu Ser Ala Thr Asn Glu Asn Asn  
 610 615 620  
 Thr Asn Pro Glu Pro Gln Phe Gln Thr Glu Ala Thr Gly Pro Ser Ala  
 625 630 635 640  
 His Glu Glu Thr Ser Thr Arg Asp Ser Ala Leu Gln Asp Thr Asp Asp  
 645 650 655  
 Ser Asp Asp Asp Pro Val Leu Ile Pro Gly Ala Arg Tyr Arg Ala Gly  
 660 665 670  
 Pro Gly Asp Arg Arg Ser Ala Val Ala Arg Ile Gln Glu Phe Phe Arg  
 675 680 685  
 Arg Arg Lys Glu Arg Lys Glu Met Glu Glu Leu Asp Thr Leu Asn Ile  
 690 695 700  
 Arg Arg Pro Leu Val Lys Met Val Tyr Lys Gly His Arg Asn Ser Arg  
 705 710 715 720  
 Thr Met Ile Lys Glu Ala Asn Phe Trp Gly Ala Asn Phe Val Met Ser  
 725 730 735  
 Gly Ser Asp Cys Gly His Ile Phe Ile Trp Asp Arg His Thr Ala Glu  
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His Tyr Gly Thr Thr Tyr Glu Ile Met Thr Val Pro Asn Asp Pro Tyr	
140 145 150 155	
act ttt ctc tct tgt ggt gaa gat gga act gtt agg tgg ttt gat aca	530
Thr Phe Leu Ser Cys Gly Glu Asp Gly Thr Val Arg Trp Phe Asp Thr	
160 165 170	
cgc atc aaa act agc tgc aca aaa gaa gat tgt aaa gat gat att tta	578
Arg Ile Lys Thr Ser Cys Thr Lys Glu Asp Cys Lys Asp Asp Ile Leu	
175 180 185	
att aac tgt cga cgt gct gcc acg tct gtt gct att tgc cca cca ata	626
Ile Asn Cys Arg Arg Ala Ala Thr Ser Val Ala Ile Cys Pro Pro Ile	
190 195 200	
cca tat tac ctt gct gtt ggt tgt tct gac agc tca gta cga ata tat	674
Pro Tyr Tyr Leu Ala Val Gly Cys Ser Asp Ser Val Arg Ile Tyr	
205 210 215	
gat cgg cga atg ctg ggc aca aga gct aca ggg aat tat gca ggt cga	722
Asp Arg Arg Met Leu Gly Thr Arg Ala Thr Gly Asn Tyr Ala Gly Arg	
220 225 230 235	
ggg act act gga atg gtt gcc cgt ttt att cct tcc cat ctt aat aat	770
Gly Thr Thr Gly Met Val Ala Arg Phe Ile Pro Ser His Leu Asn Asn	
240 245 250	
aag tcc tgc aga gtg aca tct ctg tgt tac agt gaa gat ggt caa gag	818
Lys Ser Cys Arg Val Thr Ser Leu Cys Tyr Ser Glu Asp Gly Gln Glu	
255 260 265	
att ctc gtt agt tac tct tca gat tac ata tat ctt ttt gac ccg aaa	866
Ile Leu Val Ser Tyr Ser Ser Asp Tyr Ile Tyr Leu Phe Asp Pro Lys	
270 275 280	
gat gat aca gca cga gaa ctt aaa act cct tct gcg gaa gag aga aga	914
Asp Asp Thr Ala Arg Glu Leu Lys Thr Pro Ser Ala Glu Glu Arg Arg	
285 290 295	
gaa gag ttg cga caa cca cca gtt aag cgt ttg aga ctt cgt ggt gat	962
Glu Glu Leu Arg Gln Pro Pro Val Lys Arg Leu Arg Leu Arg Gly Asp	
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Trp Ser Asp Thr Gly Pro Arg Ala Arg Pro Glu Ser Glu Arg Glu Arg	
320 325 330	
gat gga gag cag agt ccc aat gtg tca ttg atg cag aga atg tct gat	1058
Asp Gly Glu Gln Ser Pro Asn Val Ser Leu Met Gln Arg Met Ser Asp	
335 340 345	
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att tca act ctt cct acg gtc cca tca agt cct gat ttg gaa gtg agt Ile Ser Thr Leu Pro Thr Val Pro Ser Ser Pro Asp Leu Glu Val Ser 380 385 390 395			1202
gaa act gca atg gaa gta gat act cca gct gaa caa ttt ctt cag cct Glu Thr Ala Met Glu Val Asp Thr Pro Ala Glu Gln Phe Leu Gln Pro 400 405 410			1250
tct aca tcc tct aca atg tca gct cag gct cat tcg aca tca tct ccc Ser Thr Ser Ser Thr Met Ser Ala Gln Ala His Ser Thr Ser Ser Pro 415 420 425			1298
aca gaa agc cct cat tct act cct ttg cta tct tct cca gac agt gaa Thr Glu Ser Pro His Ser Thr Pro Leu Leu Ser Ser Pro Asp Ser Glu 430 435 440			1346
caa agg cag tct gtt gag gca tct gga cac cac aca cat cat cag tct Gln Arg Gln Ser Val Glu Ala Ser Gly His His Thr His His Gln Ser 445 450 455			1394
gat aac aat aat gaa aag ctg agc ccc aaa cca ggg aca ggt gaa cca Asp Asn Asn Asn Glu Lys Leu Ser Pro Lys Pro Gly Thr Gly Glu Pro 460 465 470 475			1442
gtt tta agt ttg cac tac agc aca gaa gga aca act aca agc aca ata Val Leu Ser Leu His Tyr Ser Thr Glu Gly Thr Thr Thr Ser Thr Ile 480 485 490			1490
aaa ctg aac ttt aca gat gaa tgg agc agt ata gca tca agt tct aga Lys Leu Asn Phe Thr Asp Glu Trp Ser Ser Ile Ala Ser Ser Ser Arg 495 500 505			1538
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cca cag agc tca gtg caa cca cca gaa gga gac agt gaa aca aaa gct Pro Gln Ser Ser Val Gln Pro Pro Glu Gly Asp Ser Glu Thr Lys Ala 525 530 535			1634
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 Lys Ala Lys Glu Pro Glu Thr Ser Asp Gln Thr Ser Thr Glu Ser Ala  
 605 610 615

acc aat gaa aat aac acc aat cct gag cct cag ttc caa aca gaa gcc 1922  
 Thr Asn Glu Asn Asn Thr Asn Pro Glu Pro Gln Phe Gln Thr Glu Ala  
 620 625 630 635

act ggg cct tca gct cat gaa gaa aca tcc acc agg gac tct gct ctt 1970  
 Thr Gly Pro Ser Ala His Glu Glu Thr Ser Thr Arg Asp Ser Ala Leu  
 640 645 650

cag gac aca gat gac agt gat gat gac cca gtc ctg atc cca ggt gca 2018  
 Gln Asp Thr Asp Asp Ser Asp Asp Asp Pro Val Leu Ile Pro Gly Ala  
 655 660 665

agg tat cga gca gga cct ggt gat aga cgc tct gct gtt gcc cgt att 2066  
 Arg Tyr Arg Ala Gly Pro Gly Asp Arg Arg Ser Ala Val Ala Arg Ile  
 670 675 680

cag gag ttc ttc aga cgg aga aaa gaa agg aaa gaa atg gaa gaa ttg 2114  
 Gln Glu Phe Phe Arg Arg Lys Glu Arg Lys Glu Met Glu Glu Leu  
 685 690 695

gat act ttg aac att aga agg ccg cta gta aaa atg gtt tat aaa ggc 2162  
 Asp Thr Leu Asn Ile Arg Arg Pro Leu Val Lys Met Val Tyr Lys Gly  
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 720 725 730

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 Arg His Thr Ala Glu His Leu Met Leu Leu Glu Ala Asp Asn His Val  
 750 755 760

gta aac tgc ctg cag cca cat ccg ttt gac cca att tta gcc tca tct 2354  
 Val Asn Cys Leu Gln Pro His Pro Phe Asp Pro Ile Leu Ala Ser Ser  
 765 770 775

ggc ata gat tat gac ata aag atc tgg tca cca tta gaa gag tca agg 2402  
 Gly Ile Asp Tyr Asp Ile Lys Ile Trp Ser Pro Leu Glu Glu Ser Arg  
 780 785 790 795

att ttt aac cga aaa ctt gct gat gaa gtt ata act cga aac gaa ctc 2450  
 Ile Phe Asn Arg Lys Leu Ala Asp Glu Val Ile Thr Arg Asn Glu Leu  
 800 805 810

a1  
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atg ctg gaa gaa act aga aac acc att aca gtt cca gcc tct ttc atg 2498  
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ttg agg atg ttg gct tca ctt aat cat atc cga gct gac cgg ttg gag 2546  
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                   830                                  835                                  840

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 Gly Asp Arg Ser Glu Gly Ser Gly Gln Glu Asn Glu Asn Glu Asp Glu  
                   845                                  850                                  855

gaa taataaactc tttttggcaa gcacttaaatt gttctgaaat ttgtataaga 2647  
 Glu  
 860

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16

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16

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27

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22

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a!  
Cont

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57

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27

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<213> Artificial Sequence

<220>

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